

Figure S1. Pie charts of 4036 intersected DEGs overlapping across the four datasets.

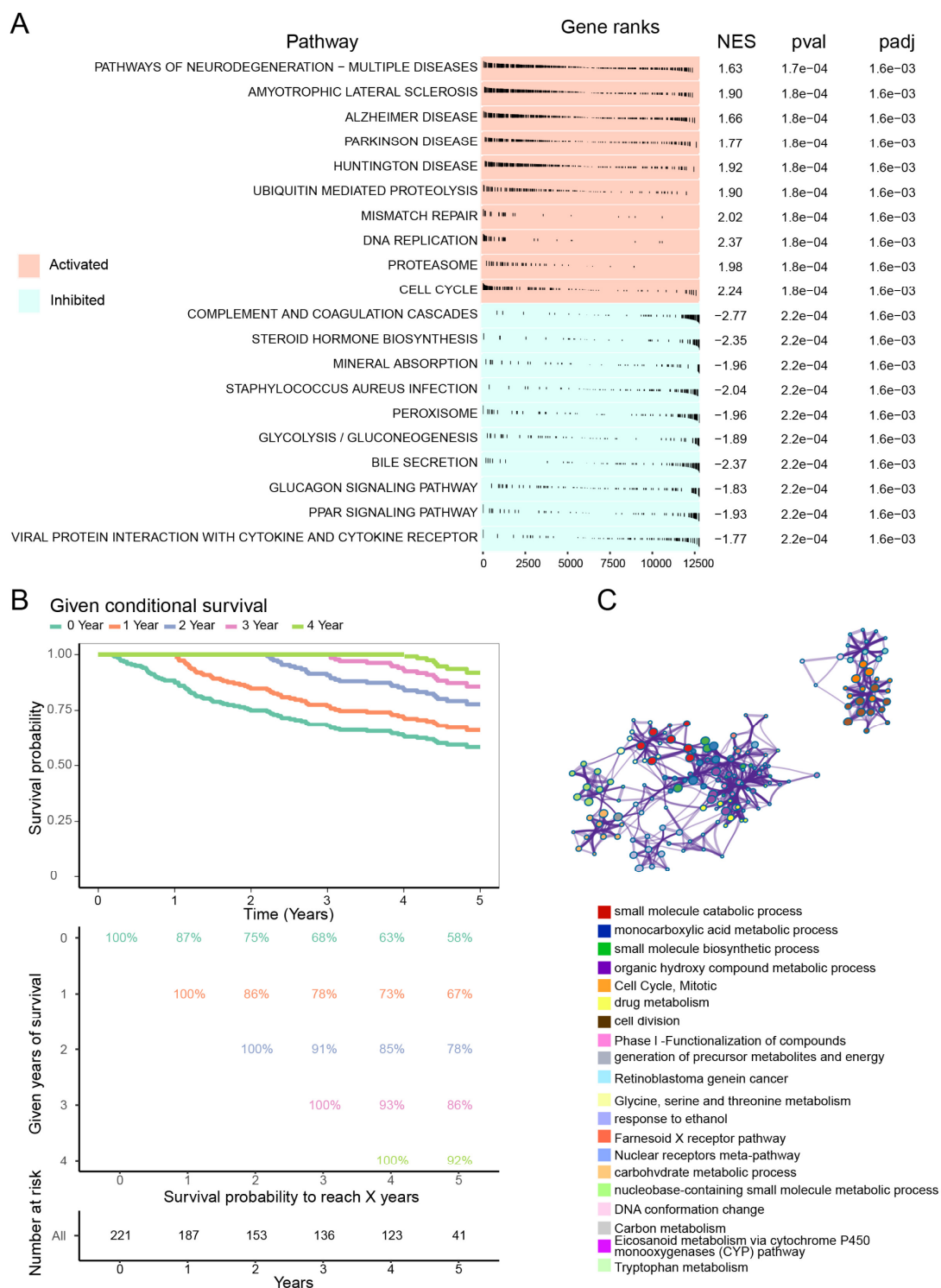


Figure S2. Gene set enrichment analysis and survival analysis of hepatocellular carcinoma (HCC) samples. (A) Top 10 pathways positively (red) or negatively (blue) correlated with DEGs. **(B)** Kaplan-Meier estimates for conditional survival in HCC

patients in GSE14520, assuming a survival rate of 100% at 0–5 years after HCC resection. (C) Gene ontology enrichment analysis of the 217 prognostic genes. Each colored dot represents a different biological process.

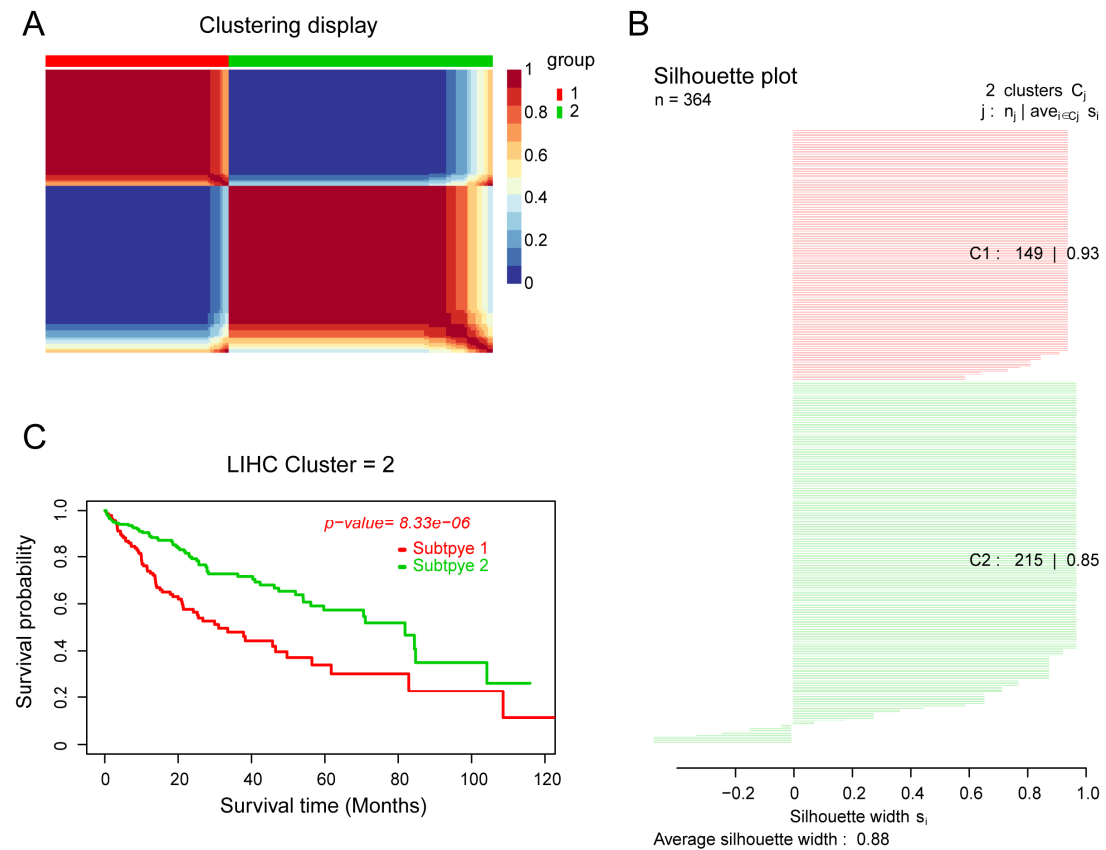


Figure S3. Identification of hepatocellular carcinoma (HCC) subtypes based on the TCGA dataset. (A) HCC samples were clustered by non-negative matrix factorization. (B) Silhouette width plots. (C) Evaluation of the different survival patterns between subtypes by the *CancerSubtypes* package. TCGA, The Cancer Genome Atlas.

expression in the (C) GSE138178 and (D) GSE84006 datasets. (E) FANCI mRNA expression in liver cancer and normal tissues based on the Oncomine database. The number in each cell represents the number of datasets. (F) FANCI expression levels in tumor and adjacent normal tissues based on RNA sequencing data from The Cancer Genome Atlas in the Tumor Immune Estimation Resource database. $P < 0.1$, $^*P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.001$.

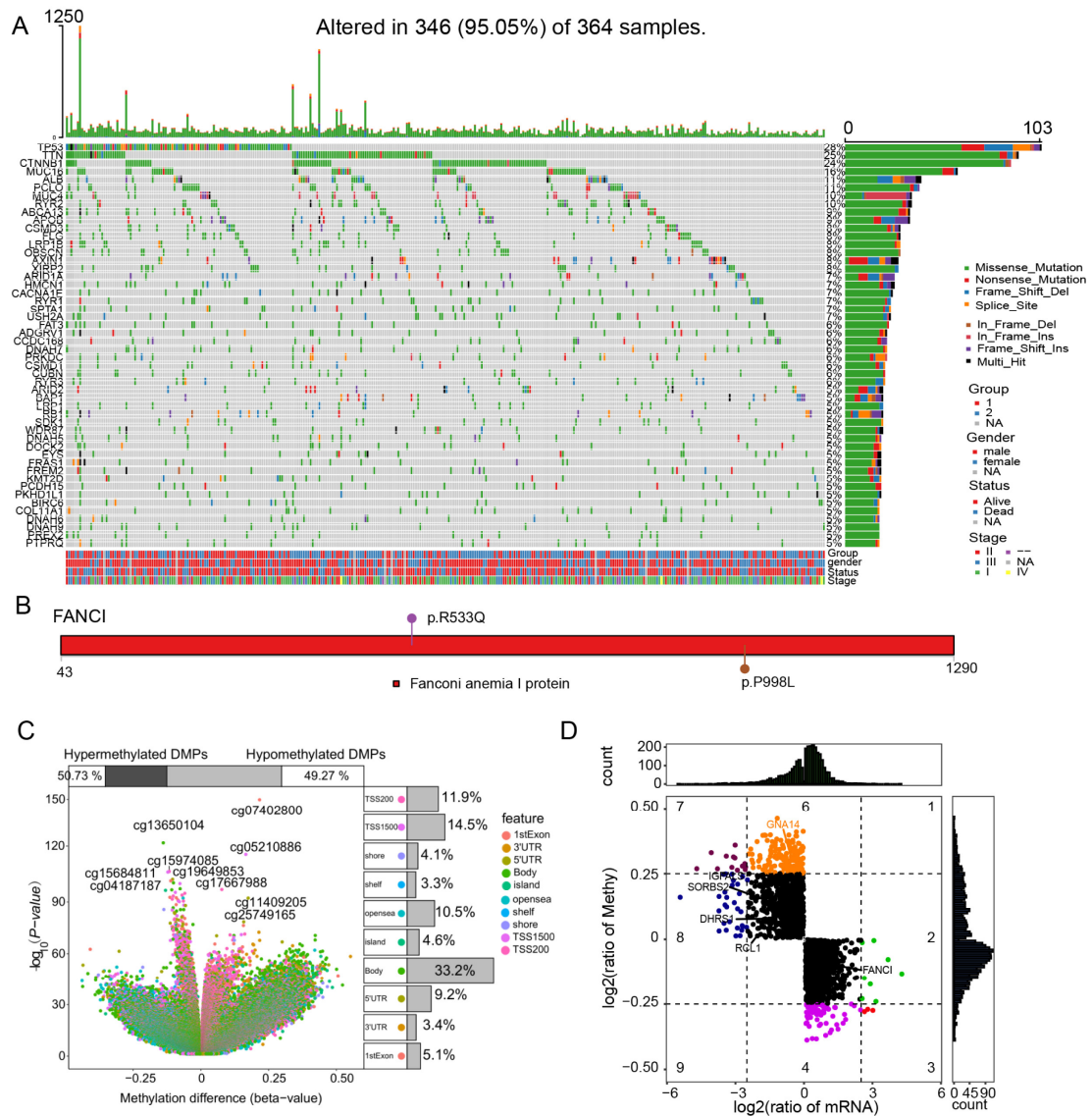


Figure S5. Genomic landscape of hepatocellular carcinoma and DNA methylation changes. (A) Waterfall plot of somatic mutations in DEGs overlapping across the GSE14520, GSE76427, GSE25097, and TCGA datasets. (B) Lollipop graph showing the mutation sites in FANCI in hepatocellular carcinoma. (C) Differentially methylated positions (DMPs) of HCC and non-tumor liver tissues obtained from Peruvian hepatocellular carcinoma patients in the GSE136319 dataset. (D) Correlation of FANCI mRNA and protein expression. TCGA, The Cancer

Genome Atlas.

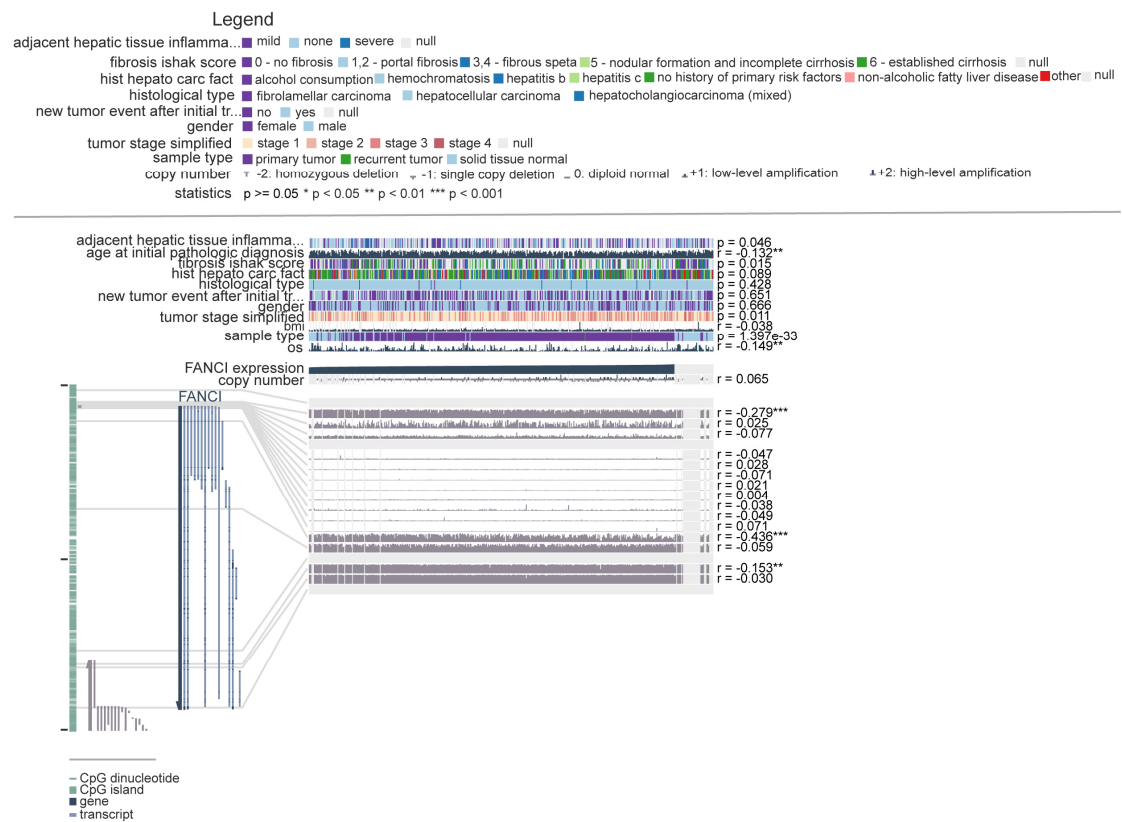


Figure S6. Correlation of FANCI expression and methylation status in hepatocellular carcinoma samples from The Cancer Genome Atlas, as determined by the MEXPRESS tool.